



SEQUENCE LISTING

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<120> METHODS FOR IDENTIFYING G-PROTEIN
COUPLED RECEPTORS ASSOCIATED WITH DISEASES

<130> 433112000700

<140> US 10/032,106

<141> 2001-12-21

<150> US 60/258,070

<151> 2000-12-20

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 924

<212> DNA

<213> Homo sapiens

<400> 1

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tggcaaggttc tcttcttcat catctttctt gtggcttaca tcataccat ggtgggcaat	120
atccggcatga tggtgttaat caaggtcagt cctcagctta acaacccat gtacttttc	180
ctcagtcact tgtcatttgc tgatgtgtgg ttttcttcca atgtcacccc taaaatgttg	240
gaaaacctgt ttccagataa aaaaacaatt acttatgctg gttgttagt acagtgttcc	300
tttccatttgc ctcttgcata tttttttttt ctgcgtatggc ctttgataga	360
tacatggcaa ttggaaatcc tctgctttat ggcagtaaaa tgtcaagggt tgcgtgtatt	420
cgtactgatta ctcccttta cattatggt tttctgacga gtctggcagc aacattatgg	480
acttacggct tgtacttctg tgaaaaatt gagatcaacc atttctactg tgcagatcca	540
cctctcatca aaatggcctg tgccgggacc tttgtaaaag aatataacaat gatcataactt	600
gccggcatta acttcacata ttccctgact gtaattatca tctcttactt attcatcctc	660
attgccattt tgcgaatgcg ctcagcagaa ggaaggcaga aggccttttc cacatgtggg	720
tcccatctga cagctgtcat tatattctat ggtactctga tcttcatgtt tctcagacgt	780
cccacagagg agtctgtgga gcaggggaag atgggtggctg ttttctatac cacagtgtac	840
cccatgttga atccccatgtt ctacagtctg aggaacaagg atgtgaaaaa ggccatgtatg	900
aaagtatca gcagatcatg tttaa	924

<210> 2

<211> 939

<212> DNA

<213> Homo sapiens

<400> 2

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cctcagctgg agctagtctt ctttgtgggt cttttgatct tctatatctt cactttgctg	120
ggaaacaaaa ccatcattgt attatctcac ttggacccac atcttcacac tcctatgtat	180
tttttcttctt ccaacctaag ctttttggat ctgtgttaca caaccggcat tgccacag	240
ctcctggta atctcaggagg agcagacaaa tcaatctcct atgggtggtg tgcgtatcag	300

ctgtacatct	ctctaggcct	gggatctaca	gaatgcgttc	tcttaggagt	gatggtattt	360
gaccgctatg	cagctgtttg	caggcccctc	cactacacag	tagtcatgca	cccttgtctg	420
tatgtgctga	tggcttctac	ttcatgggtc	attgggtttt	ccaactccct	attgcagacg	480
gtgctcatct	tgcttttaac	actttgtgga	agaaaataaaat	tagaacactt	tctttgtgag	540
gttcctccat	tgctcaagct	tgcctgtgtt	gacactacta	tgaatgaatc	tgaactcttc	600
tttgcgttg	tcattattct	tcttgtacct	gttgcattaa	tcatattctc	ctatagtcag	660
attgtcaggg	cagtcatgag	gataaagtta	gcaacagggc	agagaaaagt	gtttgggaca	720
tgtggctccc	acctcacagt	ggtttccctg	ttctacggca	cagctatcta	tgcttacctc	780
cagccccggca	acaactactc	tcaggatcag	ggcaagttca	tctctctctt	ctacaccatc	840
attacaccca	tgatcaaccc	cctcatatat	acactgagga	acaaggatgt	gaaaggagca	900
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<210> 3
<211> 930
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(930)
<223> n= a, c, g, or t
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<400> 3
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ggaaacctgg gcatgatcac tctaatttgt ctgaactctc agctgcacac ccccatgtac    180
tactttctca gcaatctgtc actcatggat ctctgctact cctccgtcat tacccttaag    240
atgctgggtga actttgtgtc agagaaaaac atcatctcc acgcagggtg catgtcacag    300
ctctacttct tccttggttt tgtcattgtc gagtgttaca tgctgacagt gatggcctac    360
gaccgctatg ttgnncntctg ccacccttg ctttacaaca tcattatgtc tcataccacc    420
tgcctgctgc tgggtggctgt ggtctacgcc atcggactca ttggctccac aatagaaaact    480
ggccctcatgt taaaactgcc ctattgttag cacctcatca gtcactactt ctgtgacatc    540
ctccctctca tgaagctgtc ctgctcttagc acctatgtat ttgagatgac agtcttctt    600
tcggctggat tcaacatcat agtcacgac ttaacagttc ttgtttctta cacccattt     660
ctctccagca tcctccggcat cagcaccaca gagggggagat ccaaaggctt cagcacctgc    720
agctccacc ttgcagccgt ggaaatgttc tatggatcaa ctgcattcat gtacttaaaa    780
ccctccacaa tcagttccctt gaccaggag aatgtggcct ctgtgttcta caccacggta    840
atccccatgt tgaatccccctt aatctacagc ctgaggaaca aggaagtaaa ggctgcccgtg    900
cagaaaacgc tgaggggtaa actgttttga                                930

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<210> 4
<211> 927
<212> DNA
<213> Homo sapiens

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<400> 4
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cctcaatgga gagacacgtt tttcacatta gtgctgataa ttacacctcg cacattgttg     120
ggaaatggat ttatgatctt tcttatttcac ttgacccccaa acctccacac tccaatctac     180
ttcttccta gtaacctgtc tttcttagac ctttgttatg gaacagcttc catgcccag     240
gctttggtgc attgtttctc tacccatccc tacctctctt atccccgatg tttggctcaa     300
acgagtgtct ccttggcttt ggccacagca gagtgcctcc tactggctgc catggcctat     360
gaccgtgtgg ttgctatcag caatccctcg cgttatttcag tggttatgaa tggcccgata    420
tgtgtctgtc tgggtgctac ctcatggggg acatcaacttg tgctcaactgc catgctcatc    480
ctatccctga ggcttcactt ctgtggggct aatgtcatca accatttgc ctgtgagatt     540
ctctccctca ttaagctgac ctgttctgtat accagcctca atgaatttat gatcctcatc     600
accagtatct tcaccctgct gctaccattt gggtttggttc tccttcctca catacgaatt    660
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gctatggcta tcataaggat tcgctcactc cagggcaggc tcaaggcctt taccacatgt	720
ggctctcacc tgaccgttgt gacaatcttc tatgggttag ccatctccat gtatatgaaa	780
actcagtcca agtccttaccc tgaccaggac aagtttatct cagtgtttta tggagcttg	840
acacccatgt tgaaccccct gatatacgc ctgagaaaaaa aagatgttaa acgggcaata	900
aggaaagtta tggaaaag gacatga	927

<210> 5
<211> 945
<212> DNA
<213> Homo sapiens

<400> 5	
atgtcagcct ccaatatcac ctaaacacat ccaactgcct tcttgggtt ggggattcca	60
ggcctggAAC acctgcacat ctggatctcc atccctttct gcttagcata tacactggcc	120
ctgcttggAA actgcactct cttcttcattt atccaggctg atgcagccct ccatgaaccc	180
atgtacctct ttctggccat gttggcagcc atcgacctgg tcctttccctc ctcagcactg	240
cccaaaatgc ttgccccattt ctgggtcagg gatcgggaga taaaacttctt tgcctgtctg	300
gccagatgt tcttccttca ctcccttcattt atcatggagt cagcagtgt gctggccatg	360
gccttggacc gctatgtggc tatctgcaag ccactgcact acaccaaggc cctgactggg	420
tccctcatca ccaagattgg catggctgtt gttggccggg ctgtgacact aatgactcca	480
ctcccttcc ttctggatgt ttccactac tgccgaggcc cagtgatcgc tcactgctac	540
tgtgaacaca tggctgtggt gaggctggcg tgggggaca ctggcttcaa caaatatctat	600
ggcatcgctg tggccatgtt tattgtgggtt ttggacactgc tccttggat tctgtcttat	660
atctttatcc ttctggatgt ttctgtcatat aggtgccatc ttggccatgtt acaccaactgt ggtcatctct	720
tcagtcatgc accgtgttagc ccggccatgtt gcccctcatg tccacatctt ccttggccat	780
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	945

<210> 6
<211> 307
<212> PRT
<213> Homo sapiens

<400> 6	
Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu Thr	
1 5 10 15	
Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Ile Phe Leu Val Val	
20 25 30	
Tyr Ile Ile Thr Met Val Gly Asn Ile Gly Met Met Val Leu Ile Lys	
35 40 45	
Val Ser Pro Gln Leu Asn Asn Pro Met Tyr Phe Phe Leu Ser His Leu	
50 55 60	
Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met Leu	
65 70 75 80	
Glu Asn Leu Phe Ser Asp Lys Lys Thr Ile Thr Tyr Ala Gly Cys Leu	
85 90 95	
Val Gln Cys Phe Phe Ile Ala Leu Val His Val Glu Ile Phe Ile	
100 105 110	
Leu Ala Ala Met Ala Phe Asp Arg Tyr Met Ala Ile Gly Asn Pro Leu	
115 120 125	
Leu Tyr Gly Ser Lys Met Ser Arg Val Val Cys Ile Arg Leu Ile Thr	
130 135 140	
Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Ala Ala Thr Leu Trp	
145 150 155 160	
Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His Phe Tyr	
165 170 175	

Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr Phe Val
180 185 190
Lys Glu Tyr Thr Met Ile Ile Leu Ala Gly Ile Asn Phe Thr Tyr Ser
195 200 205
Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala Ile Leu
210 215 220
Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Gly
225 230 235 240
Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile Phe Met
245 250 255
Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val
260 265 270
Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr
275 280 285
Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val Ile Ser
290 295 300
Arg Ser Cys
305

<210> 7
<211> 312
<212> PRT
<213> Homo sapiens

<400> 7
Met Asp Gln Lys Asn Gly Ser Ser Phe Thr Gly Phe Ile Leu Leu Gly
1 5 10 15
Phe Ser Asp Arg Pro Gln Leu Glu Leu Val Leu Phe Val Val Leu Leu
20 25 30
Ile Phe Tyr Ile Phe Thr Leu Leu Gly Asn Lys Thr Ile Ile Val Leu
35 40 45
Ser His Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Phe Ser
50 55 60
Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Gly Ile Val Pro Gln
65 70 75 80
Leu Leu Val Asn Leu Arg Gly Ala Asp Lys Ser Ile Ser Tyr Gly Gly
85 90 95
Cys Val Val Gln Leu Tyr Ile Ser Leu Gly Leu Gly Ser Thr Glu Cys
100 105 110
Val Leu Leu Gly Val Met Val Phe Asp Arg Tyr Ala Ala Val Cys Arg
115 120 125
Pro Leu His Tyr Thr Val Val Met His Pro Cys Leu Tyr Val Leu Met
130 135 140
Ala Ser Thr Ser Trp Val Ile Gly Phe Ala Asn Ser Leu Leu Gln Thr
145 150 155 160
Val Leu Ile Leu Leu Leu Thr Leu Cys Gly Arg Asn Lys Leu Glu His
165 170 175
Phe Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Val Asp Thr
180 185 190
Thr Met Asn Glu Ser Glu Leu Phe Phe Val Ser Val Ile Ile Leu Leu
195 200 205
Val Pro Val Ala Leu Ile Ile Phe Ser Tyr Ser Gln Ile Val Arg Ala
210 215 220
Val Met Arg Ile Lys Leu Ala Thr Gly Gln Arg Lys Val Phe Gly Thr
225 230 235 240
Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
245 250 255

Tyr Ala Tyr Leu Gln Pro Gly Asn Asn Tyr Ser Gln Asp Gln Gly Lys
260 265 270
Phe Ile Ser Leu Phe Tyr Thr Ile Ile Thr Pro Met Ile Asn Pro Leu
275 280 285
Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Lys Val
290 295 300
Leu Trp Lys Asn Tyr Asp Ser Arg
305 310

<210> 8
<211> 309
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(309)
<223> Xaa= any amino acid

<400> 8
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Leu Thr Lys Arg Ala Asp Leu Gln Leu Pro Leu Phe Leu Phe Leu
20 25 30
Gly Ile Tyr Leu Val Thr Ile Val Gly Asn Leu Gly Met Ile Thr Leu
35 40 45
Ile Cys Leu Asn Ser Gln Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
50 55 60
Asn Leu Ser Leu Met Asp Leu Cys Tyr Ser Ser Val Ile Thr Pro Lys
65 70 75 80
Met Leu Val Asn Phe Val Ser Glu Lys Asn Ile Ile Ser Tyr Ala Gly
85 90 95
Cys Met Ser Gln Leu Tyr Phe Leu Val Phe Val Ile Ala Glu Cys
100 105 110
Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Xaa Xaa Cys His
115 120 125
Pro Leu Leu Tyr Asn Ile Ile Met Ser His His Thr Cys Leu Leu Leu
130 135 140
Val Ala Val Val Tyr Ala Ile Gly Leu Ile Gly Ser Thr Ile Glu Thr
145 150 155 160
Gly Leu Met Leu Lys Leu Pro Tyr Cys Glu His Leu Ile Ser His Tyr
165 170 175
Phe Cys Asp Ile Leu Pro Leu Met Lys Leu Ser Cys Ser Ser Thr Tyr
180 185 190
Asp Val Glu Met Thr Val Phe Phe Ser Ala Gly Phe Asn Ile Ile Val
195 200 205
Thr Ser Leu Thr Val Leu Val Ser Tyr Thr Phe Ile Leu Ser Ser Ile
210 215 220
Leu Gly Ile Ser Thr Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
225 230 235 240
Ser Ser His Leu Ala Ala Val Gly Met Phe Tyr Gly Ser Thr Ala Phe
245 250 255
Met Tyr Leu Lys Pro Ser Thr Ile Ser Ser Leu Thr Gln Glu Asn Val
260 265 270
Ala Ser Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Leu Ile
275 280 285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Ala Ala Val Gln Lys Thr Leu

290
Arg Gly Lys Leu Phe
305

<210> 9
<211> 308
<212> PRT
<213> Homo sapiens

<400> 9
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Ile Ser Asn Tyr Pro Gln Trp Arg Asp Thr Phe Phe Thr Leu Val Leu
20 25 30
Ile Ile Tyr Leu Ser Thr Leu Leu Gly Asn Gly Phe Met Ile Phe Leu
35 40 45
Ile His Phe Asp Pro Asn Leu His Thr Pro Ile Tyr Phe Phe Leu Ser
50 55 60
Asn Leu Ser Phe Leu Asp Leu Cys Tyr Gly Thr Ala Ser Met Pro Gln
65 70 75 80
Ala Leu Val His Cys Phe Ser Thr His Pro Tyr Leu Ser Tyr Pro Arg
85 90 95
Cys Leu Ala Gln Thr Ser Val Ser Leu Ala Leu Ala Thr Ala Glu Cys
100 105 110
Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Val Val Ala Ile Ser Asn
115 120 125
Pro Leu Arg Tyr Ser Val Val Met Asn Gly Pro Val Cys Val Cys Leu
130 135 140
Val Ala Thr Ser Trp Gly Thr Ser Leu Val Leu Thr Ala Met Leu Ile
145 150 155 160
Leu Ser Leu Arg Leu His Phe Cys Gly Ala Asn Val Ile Asn His Phe
165 170 175
Ala Cys Glu Ile Leu Ser Leu Ile Lys Leu Thr Cys Ser Asp Thr Ser
180 185 190
Leu Asn Glu Phe Met Ile Leu Ile Thr Ser Ile Phe Thr Leu Leu Leu
195 200 205
Pro Phe Gly Phe Val Leu Leu Ser Tyr Ile Arg Ile Ala Met Ala Ile
210 215 220
Ile Arg Ile Arg Ser Leu Gln Gly Arg Leu Lys Ala Phe Thr Thr Cys
225 230 235 240
Gly Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Ser Ala Ile Ser
245 250 255
Met Tyr Met Lys Thr Gln Ser Lys Ser Tyr Pro Asp Gln Asp Lys Phe
260 265 270
Ile Ser Val Phe Tyr Gly Ala Leu Thr Pro Met Leu Asn Pro Leu Ile
275 280 285
Tyr Ser Leu Arg Lys Lys Asp Val Lys Arg Ala Ile Arg Lys Val Met
290 295 300
Leu Lys Arg Thr
305

<210> 10
<211> 314
<212> PRT
<213> Homo sapiens

<400> 10

Met Ser Ala Ser Asn Ile Thr Leu Thr His Pro Thr Ala Phe Leu Leu
1 5 10 15
Val Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro
20 25 30
Phe Cys Leu Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu
35 40 45
Leu Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe
50 55 60
Leu Ala Met Leu Ala Ala Ile Asp Leu Val Leu Ser Ser Ser Ala Leu
65 70 75 80
Pro Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Arg Glu Ile Asn Phe
85 90 95
Phe Ala Cys Leu Ala Gln Met Phe Phe Leu His Ser Phe Ser Ile Met
100 105 110
Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
115 120 125
Cys Lys Pro Leu His Tyr Thr Lys Val Leu Thr Gly Ser Leu Ile Thr
130 135 140
Lys Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro
145 150 155 160
Leu Pro Phe Leu Leu Arg Cys Phe His Tyr Cys Arg Gly Pro Val Ile
165 170 175
Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly
180 185 190
Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile
195 200 205
Val Val Leu Asp Leu Leu Leu Val Ile Leu Ser Tyr Ile Phe Ile Leu
210 215 220
Gln Ala Val Leu Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe
225 230 235 240
Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Thr
245 250 255
Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro
260 265 270
His Val His Ile Leu Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met
275 280 285
Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser
290 295 300
Ile Leu Gly Val Phe Pro Arg Lys Asp Met
305 310